

AKT-phosphorylated FOXO3 translocates to cytosol

Levin, ER., Rothfels, K.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 76

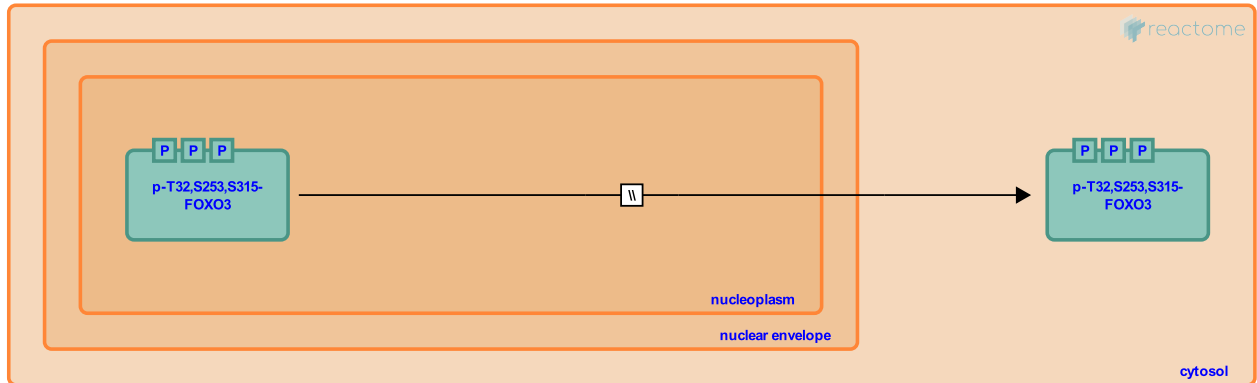
This document contains 1 reaction ([see Table of Contents](#))

AKT-phosphorylated FOXO3 translocates to cytosol ↗

Stable identifier: R-HSA-9624527

Type: omitted

Compartments: nucleoplasm, cytosol



AKT-mediated phosphorylation of FOXO3 downstream of estrogen stimulation promotes its inactivation and translocation to the cytosol, interfering with its pro-apoptotic transcription factor activity (Richards et al, 2002; Brunet et al, 1999; reviewed in Levin, 2005; Burgering, 2008).

Literature references

- Richards, JS., Sharma, SC., Falender, AE., Lo, YH. (2002). Expression of FKHR, FKHRL1, and AFX genes in the rodent ovary: evidence for regulation by IGF-I, estrogen, and the gonadotropins. *Mol. Endocrinol.*, 16, 580-99. ↗
- Levin, ER. (2005). Integration of the extranuclear and nuclear actions of estrogen. *Mol. Endocrinol.*, 19, 1951-9. ↗
- Burgering, BM. (2008). A brief introduction to FOXOlogy. *Oncogene*, 27, 2258-62. ↗
- Brunet, A., Bonni, A., Zigmond, MJ., Lin, MZ., Juo, P., Hu, LS. et al. (1999). Akt promotes cell survival by phosphorylating and inhibiting a Forkhead transcription factor. *Cell*, 96, 857-68. ↗

Editions

2018-12-15	Authored	Rothfels, K.
2019-02-20	Reviewed	Levin, ER.